

Table 1. Identification of peptides in AfC fractions.

Protein extract	CssI (AnrP440134)	Hydrophobin (AnrP57221)	GAPDH (AnrP539502)	Enolase (AnrP7789)	Catalases and IMDH B
Diffusate	KVAQEIIINPGPK	FPPVDDITVK ATYAGDVTIDEGILAGTLK	AGISLNPNFVK TAAQNTIPSSTGAAK	NVNNTGPALIK VNQIGTLTESIQAAK	Not detected
Cell surface exposed	VAQEIIINPGPK	FPPVDDITVK ATYAGDVTIDEGILAGTLK	Not detected	Not detected	FGFDLIDPTK (catalase B peptide AnrP977704) LX ₂ AEX ₂ ALR (IMDH B peptide)
1/29				TPGSLLIEDQIAR (Catalase A peptide AnrP145557)	
Cell wall	KVAQEIIINPGPK VAQEIIINPGPK SISFOLDCR EGAEQSAPOQAEHSTK VVTTPYTCQVK	FPPVDDITVK 3-12 ATYAGDVTIDEGILAGTLK 30-50 VPTSNVSVDLTCA YDTTHGQFK GTIETYDQGLIVNGK	AGISLNPNFVK TAAQNTIPSSTGAAK NLTGYTEDDVVSSDLNGDER VPTSNVSVDLTCA YDTTHGQFK GTIETYDQGLIVNGK	Not detected	
Peptides used for Ab production	KVAQEIIINPGPKVTT KEGAEQSAPOQAEHSTK	PVPDDITVKQATEKCGD ATYAGDVTIDEGIL FKGTIETYDQGLIVNGKK	KVNNETIGPALKIEND DEEDQLRFGFDLIDPTKIVP TSDFQIVGDDLTIVNPGR	RIDNDLARRVARAAGV	

Table 2. Biochemical characteristics of CssI.

	Complete	N-terminus	C-terminus
MW	28179.92	13960.38	14236.54
Residues	260	130	130
Strongly Basic (+) Amino Acids (K, R)	25	10	15
Strongly Acidic (-) Amino Acids (D, E)	33	9	24
Hydrophobic Amino Acids (A, I, L, F, W, V)	89	55	34
Polar Amino Acids (N, C, Q, S, T, Y)	70	36	34
Isoelectric Point	5.081	7.626	4.760
Charge at pH 7.0	-7.634	0.892	-8.617

Table 3. Sequence of peptides chosen for the production of multiple antigenic peptides and antisera against selected target proteins

<u>Peptide name</u>	<u>Peptide sequence</u>	<u>Parental protein</u>	<u>Reactivity vs AfC*</u>	<u>Reactivity vs AfM*</u>
GAP-B-1	FKGTIEFTYDQGLIWNGKK (SEQ ID NO:12)	GAPDH B	++	+++
GAP-B-2	TEDDVVSSDLNGERS (SEQ ID NO:11)	GAPDH B	++	++
HYD-1	PVPDDITVKQATEKCGD (SEQ ID NO:9)	hydrophobin	++	+++
HYD-2	ATYAGDVTDDEGL (SEQ ID NO:10)	hydrophobin	++	+
CAT-B-1	DEEDQLRFGFDLLDPTIKTP (SEQ ID NO:15)	Catalase B	++	++
CAT-B-2	RIDNDLARRVARAIGV (SEQ ID NO:16)	Catalase B	++	++
ENO-1	KNVNETIGPALKENID (SEQ ID NO:13)	Enolase	++	-
ENO-2	TSDFQIVGDDLTVTNPGR (SEQ ID NO:14)	Enolase	-	+
Peptide 2	KEGAEQSAPQABHSTK (SEQ ID NO:8)	CsI	+++	+++
Peptide 1	KVAQEINPGPKVYTT (SEQ ID NO:7)	CsI	++	++

*Reactivity of sera raised against the peptide against the surface of AfC or AfM

Table 4. Analysis of the ability of anti-IMDH B IgG to bind the surface of clinical isolates.

Strain Number	Original substratum	Pathogenicity (underlying disease):	Anti IMDH-B intensity	
			<u>Conidia</u>	<u>Mycelium</u>
Isolate 46640	Human Lung	Aspergilloma	++	++
IHEM 1246	Outdoor air	-----	+	+
IHEM 2494	Human sputum	Allergic Bronchopulmonar Aspergillosis	++	++
IHEM 2739	Human sinus	Mycotic sinusitis	++++	++
IHEM 2895	Human bronchoaspiration (fungal ball)	Bronchitis	+++	+
IHEM 3007	Human lung	Pulmonary aspergillosis	-	+++
IHEM 4184	Human lung biopsy	Aspergillosis (heart transplant)	-	++
IHEM 4185	Human bone	Aspergillosis (heart transplant)	-	++
IHEM 4187	Human bronchial secretions	Aspergillosis (liver transplant)	+	+
IHEM 4699	Human bronchoaspiration	Aspergillosis (bone marrow transplant)	++	+
IHEM 4750	Human lung from autopsy	Aspergillosis (liver transplant)	+++	ND
IHEM 4756	Human sputum	Aspergillosis (marrow transplant)	-	+

Figure 1. The predicted protein sequences of CssI (A), hydrophobin (B), GAPDH-B (C), enolase (D), catalase B (E), catalase A(F), and isopropylmalate dehydrogenase B (G). X₁ is S or A and X₂ is L or I.

A
 MLASFQFCILPRTYRTLLCSAGAGPLLIIQFVTVASALALAPTAVVVARQAAAFVTVNSIDVCPKVVAQEIIINPGPKVVTTP
 YTCDQVKLGHGLDVSYNF DIEPLTKDTFPYCKALKVFDNEGCLGFPTLWIPLESPLEDKC1PEHYFSDEVKSISFQLDCRE
 DAPVKKEPYGPKEGAEQSAPQAEHSTKQDAQQGSHQGQEVQNSPKQEARQGSRPAEAAPKQEAEQASEAPEKKASNPAD
 SLGLGELTKVLGFR

B
 VRFPVPDDITVKQATEKCGDQAQLSCCNKATYAGDVTIDIEGILAGTLKNLIGGGSGTEGLGLFNQCSKLDLQSPIIGIPIQ
 DLVNQKCKQNIACCQNSPSDAVRFP

C
 MATPKVGINGFGRIGRIVGLNSLSHGVDVVAVNDFIEVHYAAYMLKYDTTHQFKGTIETYDQGLIVNGKKIRFYAEKD
 PSQIPWSETGAAYIVESTGVFTTKEASAHLKGAKVIIISAPSADAPMFVMGVNNTTYTSIDIQVLSNASCTTNCLAPLA
 KVINDKFGIVEGLMTTVHSYTATQKVVDAPSNDKWRGGRTAAQNIIPSSTGAAKAVGVIPSLNGKLITGMAMRVPTSNVS
 VVDLTCRLEKGASYDEIKQAIKAASEEGELKNILGYTEDDVSSDLNGDERSSIFDAKAGISLNPNFVKLVAWYDNEW

D
 MPISKIHRSVYDSRGNPTEVDVATETGLHRAIVPSGASTGQHEAHELRGDKTQWGGKGVLKAVKNVNETIGPALIKENT
 DVKDQSKVDEFLNLDGTANKSNLGANAILGVSLAVAKAGAAEKVPLVYAHISDLAGTKKPVLPVFPQNVNLNGGSHAGGR
 AFQEPMVPPDSAPSFSSEALRQGAEVYQKLKALAKKKYQGSAGNVDEGGVAPDIQTAEEALDLITEAIEQAGYTGK
 IKIAMDVASSEFYKADVKYDLDFKNPESDPSKWLTYEQLADLYKSLAAKYPIVSIEDPFAEDDWEAWSYFYKTSDFQIVGD
 DLTVTNPGRRIKKAIELKSCNALLKVNQIGTLTESTIQAAKDSYADNWGMVMSHRSGETEDVTIADIAVGLRSGQIKTGAPCR
 SERLAKLNQILRIEELGENTVYAGSKFRATAVNL

E
 MRLTFIPSILGVANAVCPYMTGELNRRDEISDGAAAATEEFLSQYYLNDNDAFMTSDVGGPIEDQNSLSAGERGPTLLED
 IFRQKIQRFDHERVPERAVHARGAGAHGVFTSYGDFSNITAASFLAKEGKQTPVFRSTVAGSRGSSDLARDVHGFA
 TDEGNFDIVGNNIPVFFIQDAILFPDLTHAVKPRGDNEIPQAAATAHDSAWDFSQQPSTMHTLLWAMSGHGIPRSF
 RHDGFGVHTFRVFTDDGASKLVKFHWSLQKGASMVWEEAQQTSGKNPDFMRQDLHDAIEAGRYPWEELGVQIM
 DEEDQLRFGFDLDPDKIVPEEFVPIKLGKMQLNRNPRNYFAETEQVMFQPGHIVRGVDFTEDPLLQGRLFSYLD
 TQLNRHGGPNFEQLPQINPQPVVHNRRDAGQMFIPLNPHAYSPKTSVNGSPKQANQTVGDGFTAPGRTTSGKL
 VRAVSSSFEDVWSQPRLFYNSLVPAEKQFVIDAIRFENANVKS
 PVVKNNVIIQLNRIDNDLARRVARAIGVAEPEP
 DPTFYHNNKTADVGTFGTKLKKLDGLKVGVLGSVQHPGSVEGASTLRDRKLDDGVVV
 LVAERLADGVQTYSTS
 DAIQFDAVVAAGAESLFAASSFTGG
 SANSASGASSLYPTGRPLQILIDGFRFGKTVGALGSGTAALRNAGIATSRDGVYVAQS
 VTDFFANDLKEGLRTFKFLLDRFPVDH

F
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 TDQWLRVTDNDRRTGPSLLEDQIAREKIHRFDHERIPERV
 VHARGTGAFGNFKLKE
 SIEDLTYAGVLT
 DTSRNT
 P
 VFR
 STVQGS
 RGSAD
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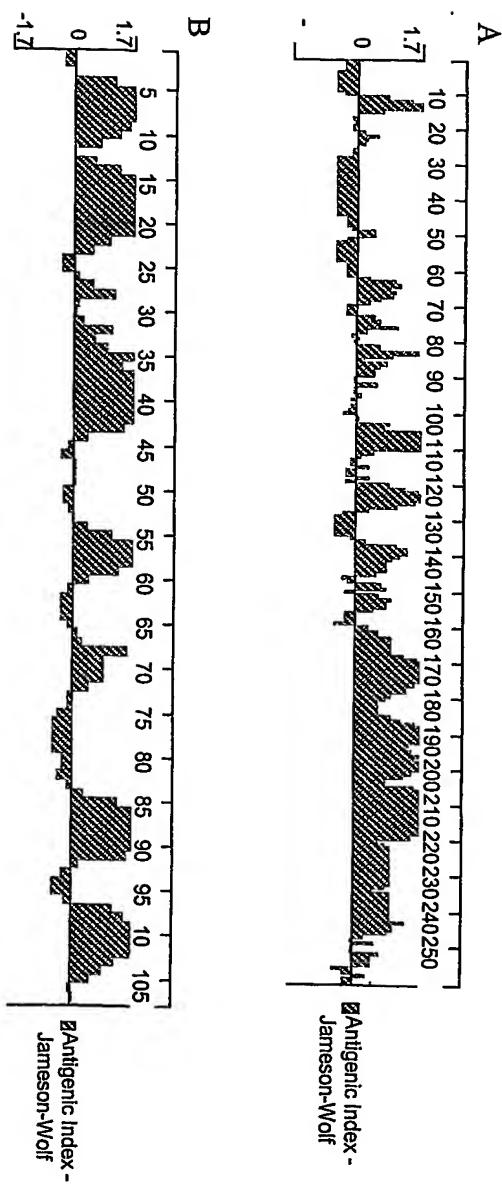
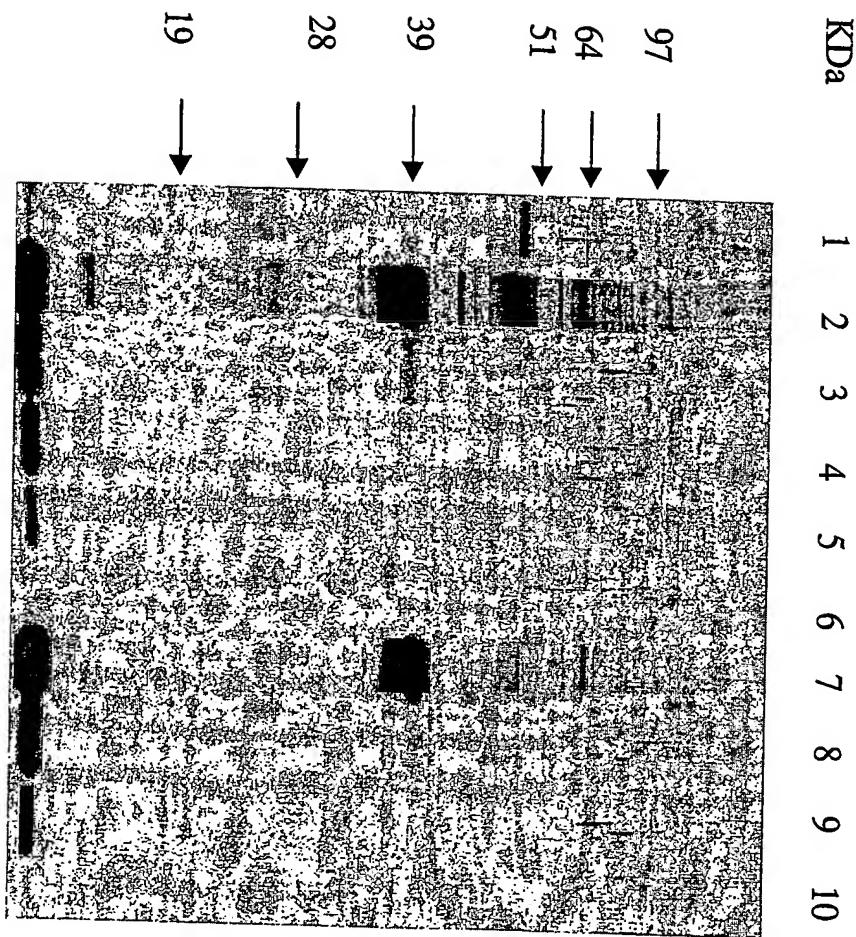


Figure 2. The predicted antigenicity indices of CssI (A) and hydrophobin (B) residues.

Figure 3. Alignment of the predicted protein sequences for GAPDH-A (AfA), GAPDH-B (AfB) and GAPDH-C (AfC).

Fig. 4



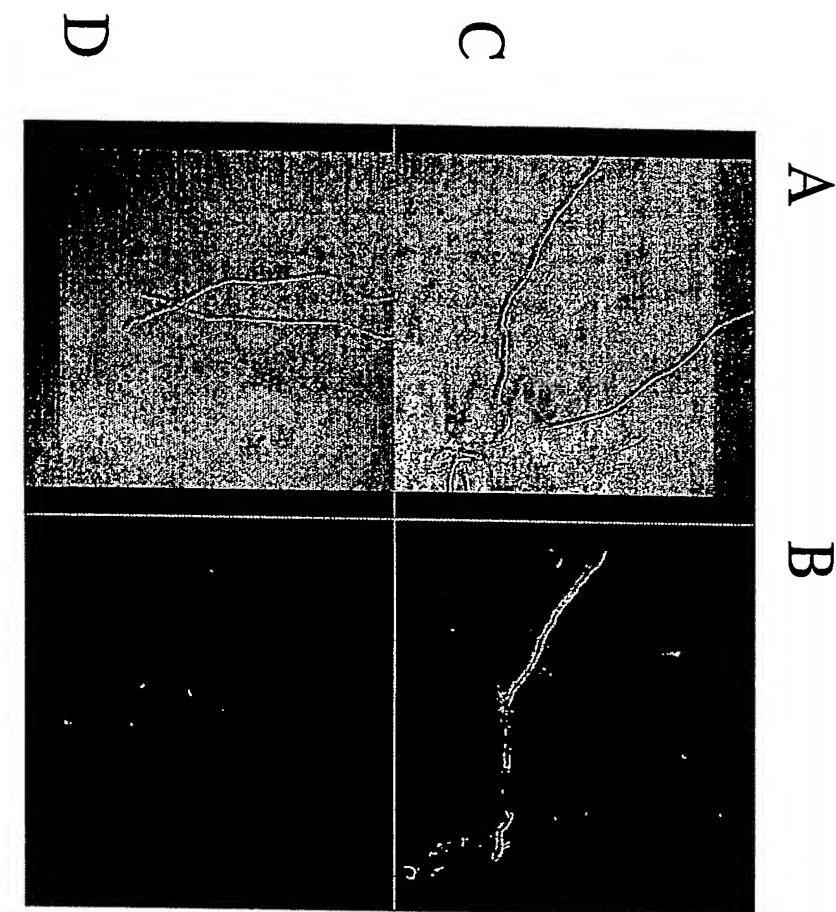


Fig. 5

Figure 6

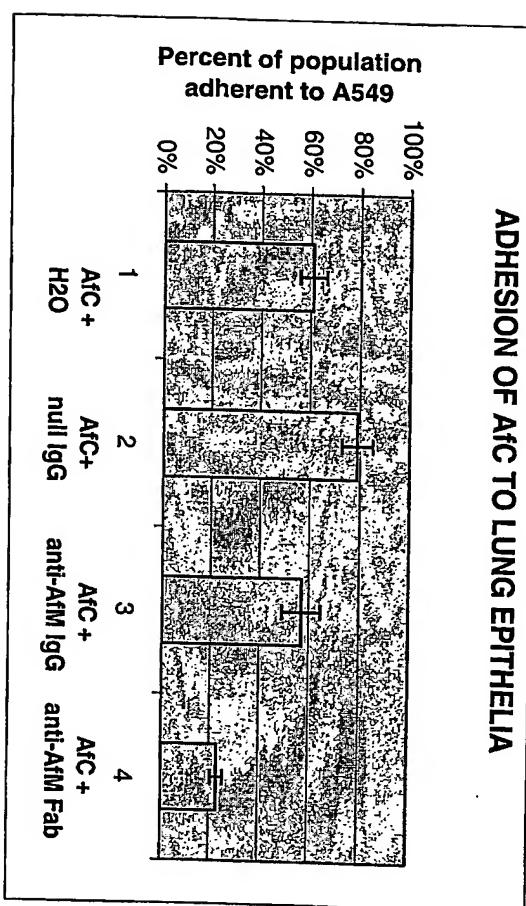
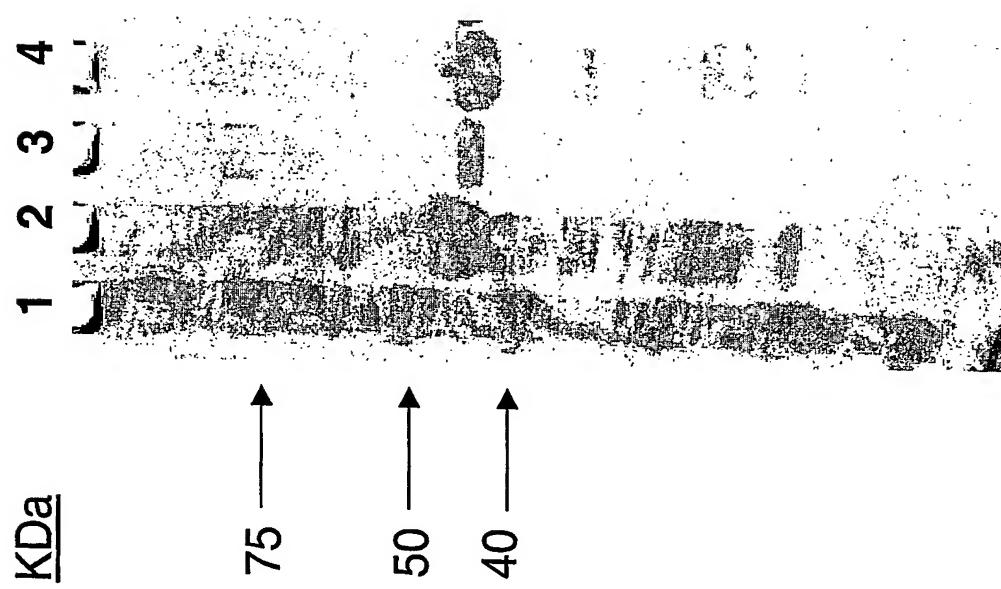


Fig. 7



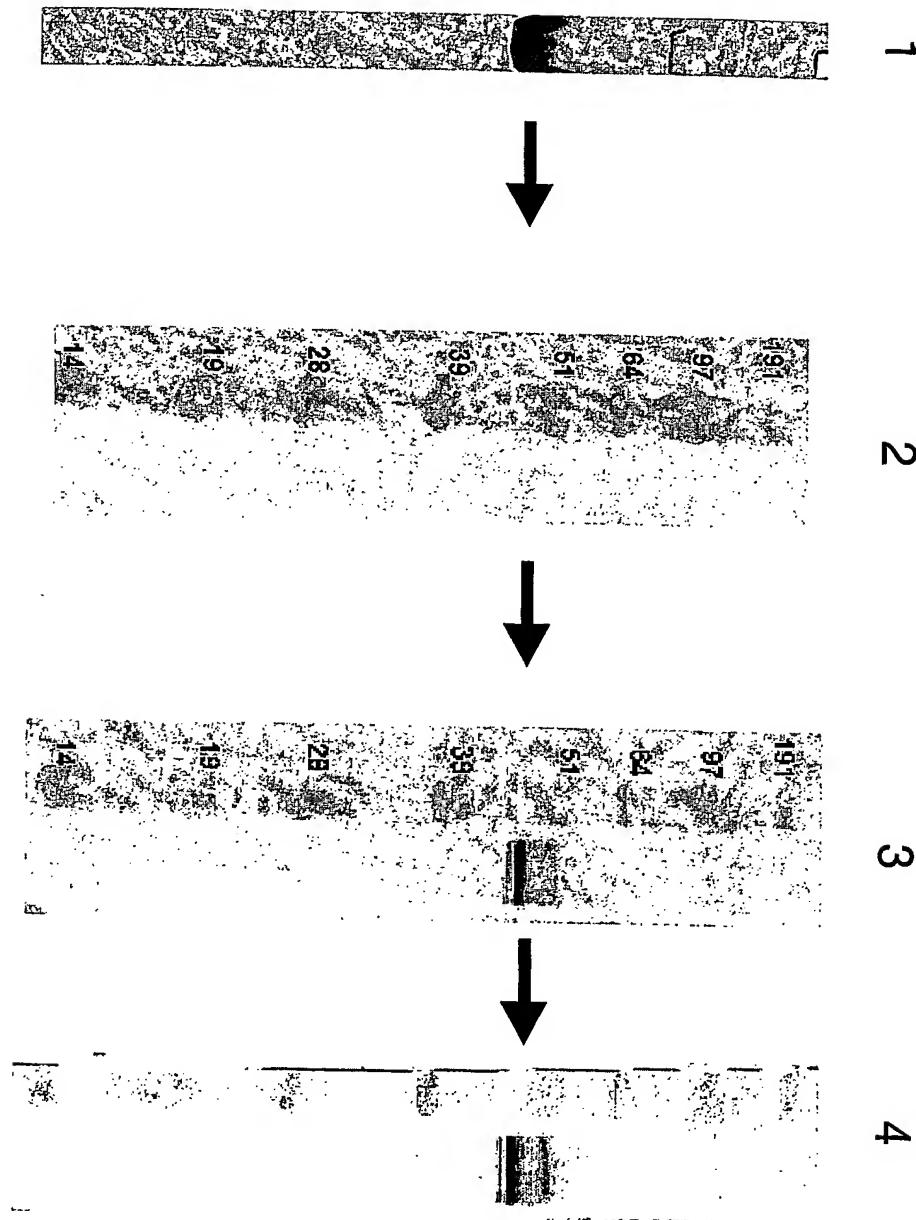


Fig. 8

Post

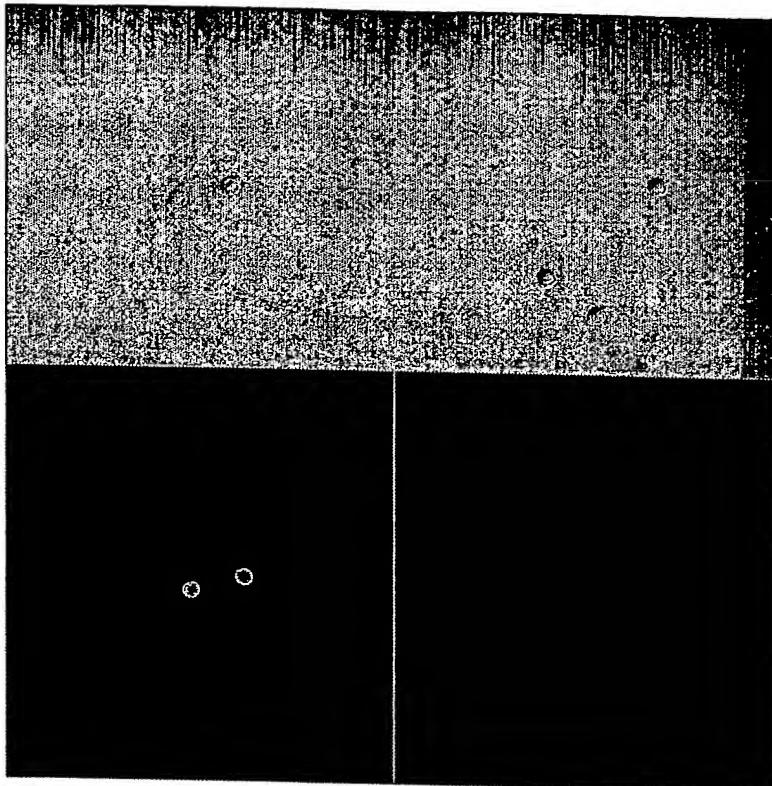


Fig. 9

Pre
AfC

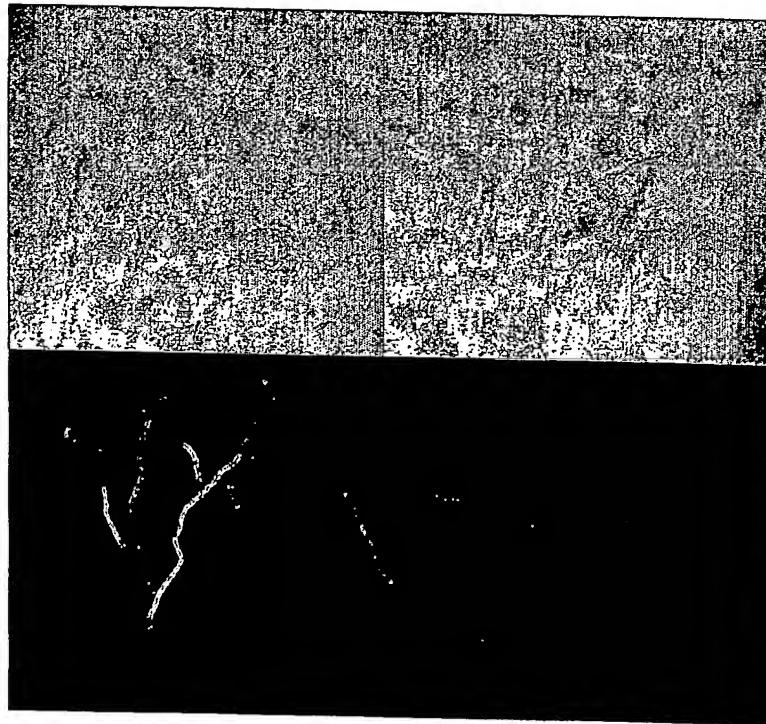


Fig. 10

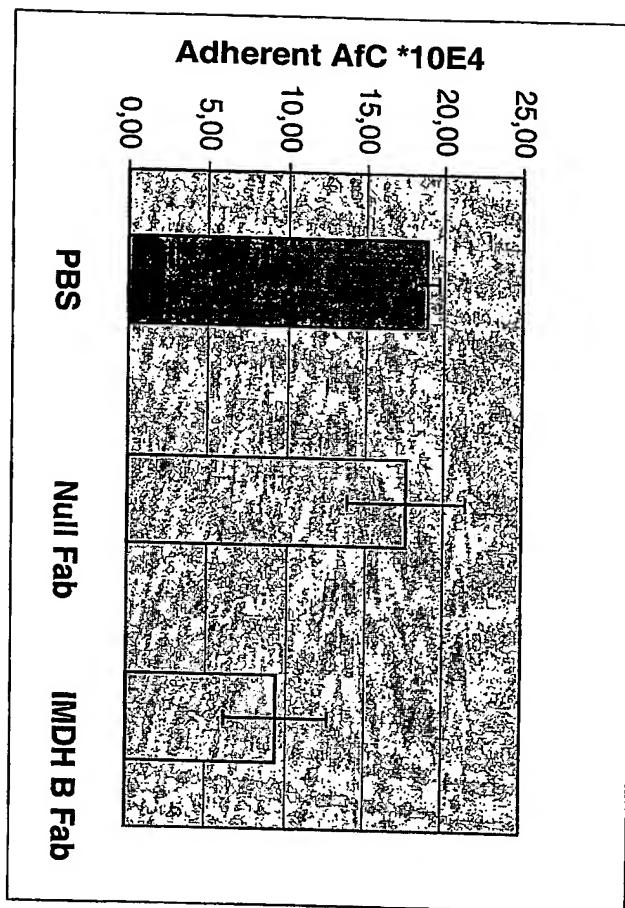


Fig. 11

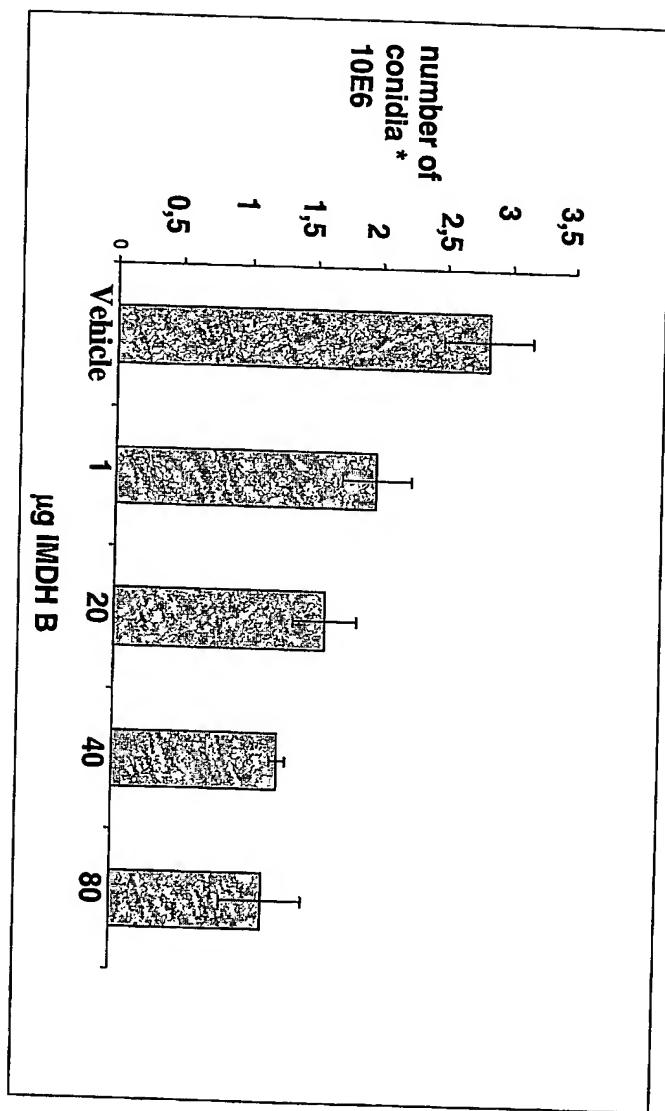


Figure 12

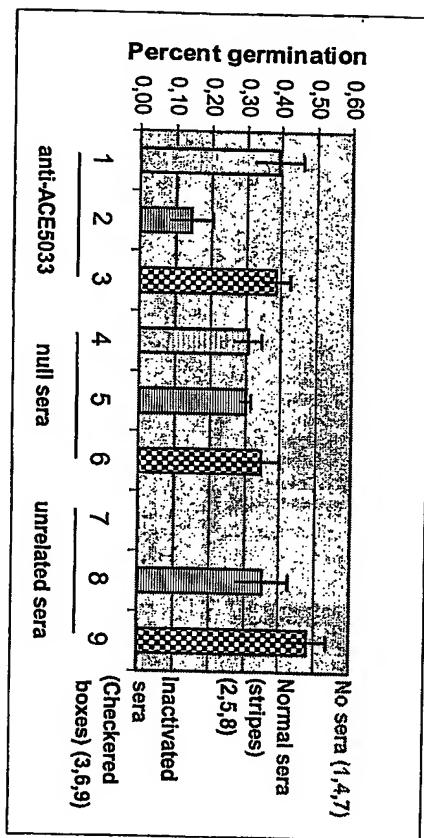


Figure 13

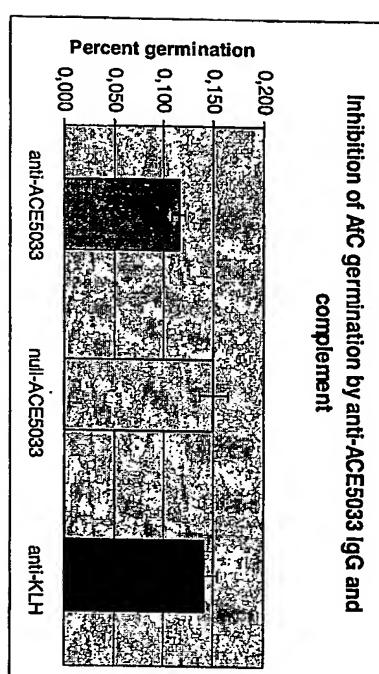


Fig. 14

IMDHB1: 3 SYNIVVFAGDHCGPEVSS----VLRVIEKCRDDATFNLQDQLLGGVSSIDATGSPLTDEA 58
 +YNI+V GD GPEV + VL+V E + FNL+ +L+GG S IDA G +T+E
 IMDHB2: 4 TYNILVLPGDGIGPEVMTEAVKVLKFEN--EHRKFNLRQELIGGCS-IDAHGKSVTEEV 60
 IMDHB1: 59 LNAAKNADAVLLGAIGGPKWG---TGAVRPEQGLLRLRKEMGTFGNLRPCNFAAPSLV-- 113
 AA +DAVL A+GGPKW G PE GLL+LRK M + NLRPC+ ++PS
 IMDHB2: 61 KKAALESDAVLFAAVGGPKWDHIRRGLDGPEGGLLQLRKAMDIYANLRPCSASSPSASIA 120
 IMDHB1: 114 -DGSPLRPEVCRGVDFNIIIRELTGGIYFGDRKEDDGSGFAMDTEPYRSRAEIERITRLAAH 172
 + SP R EV GVDF ++RE GG YFG + E++ +AMD YS EI+RITRL+A
 IMDHB2: 121 KEFSPFRQEVIEGVDFVVVRENCGGAYFGKKIEED--YAMDEWGYSEREIQRITRLSAE 178
 IMDHB1: 173 LALQHNPPLPVWSLDKANVLATSRWRKTVEVMAKEFPQLKVEHQLIDSAAMIMVKEPR 232
 +AL+HNPP PV SLDKANVLA+SRLWR+ V + M E+PQ+K+ HQL DSA++I+ PR
 IMDHB2: 179 IALRHNPWPVISLDKANVLASSRLWRRVVEKMTTEYPQVKLVHQLADSASLILATNPR 238
 IMDHB1: 233 KLNGIVVTSNLFGDIISDEASVIPGSLGLLPSASLSGIP-DGKTKVNGIYEPIHGSAPDI 291
 LNG+++ N FGD+ISD+A I G+LG+LPSASL G+P + + + NG+YEP HGSAP I
 IMDHB2: 239 ALNGVILADNTFGDMISDQAGSIVGTLGVLPSASLDGLPSETRKRTNGLYEPTHGSAPTI 298
 IMDHB1: 292 AGKGIVNPVAAILSVAMMMQYSLNRMDDARAIETAVRNIEAGIRTADIGGKSTTSEVGD 351
 AG+ I NPVA IL VA+M +YSL+ +A+ IE AV+ V++AGIRT D+GGKS T+EVGD
 IMDHB2: 299 AGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRT PDLGGKSGTNEVGD 358
 IMDHB1: 352 AVAAELE 358
 A+ A L+
 IMDHB2: 359 AIVAAALQ 365

AfC

pre

AfM

pre

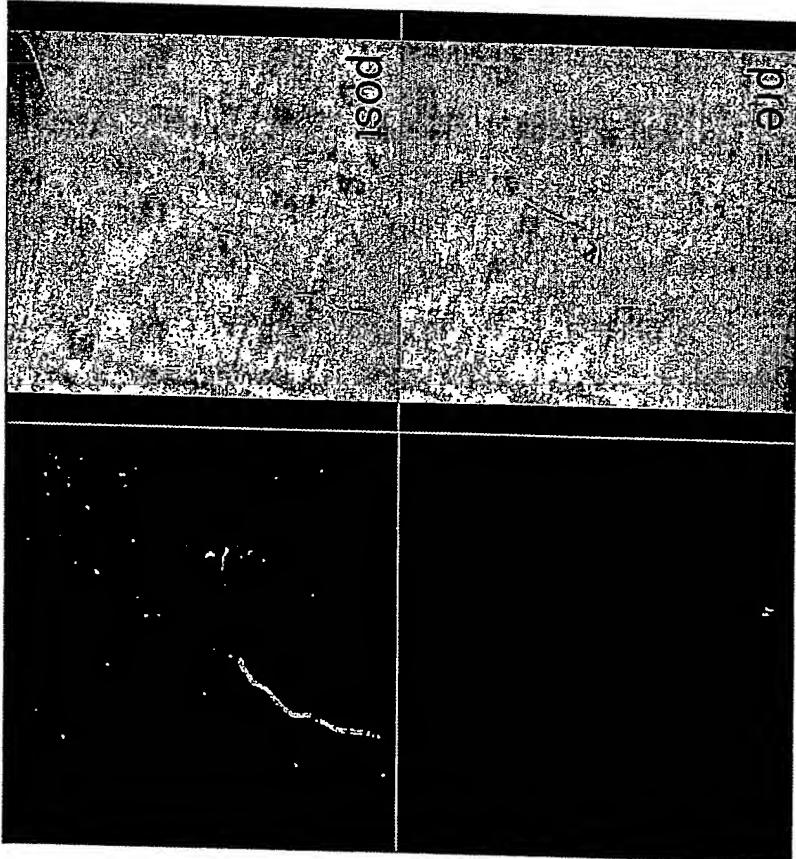
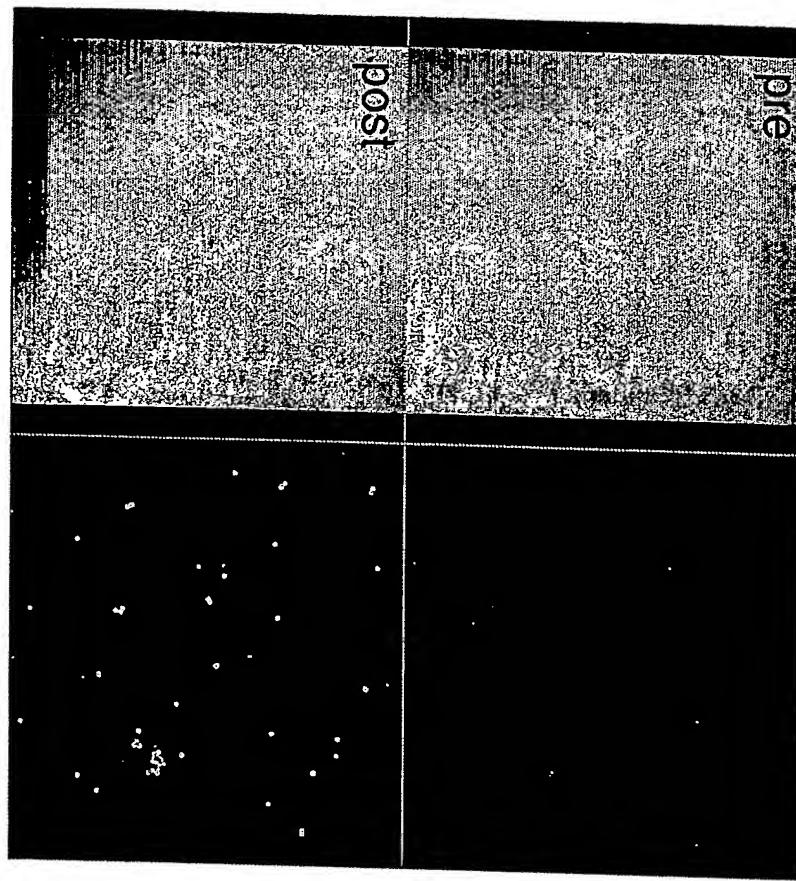


Fig. 15: Anti-GAP-B-2 (GAPDH)

Fig. 16
IHEM 3133

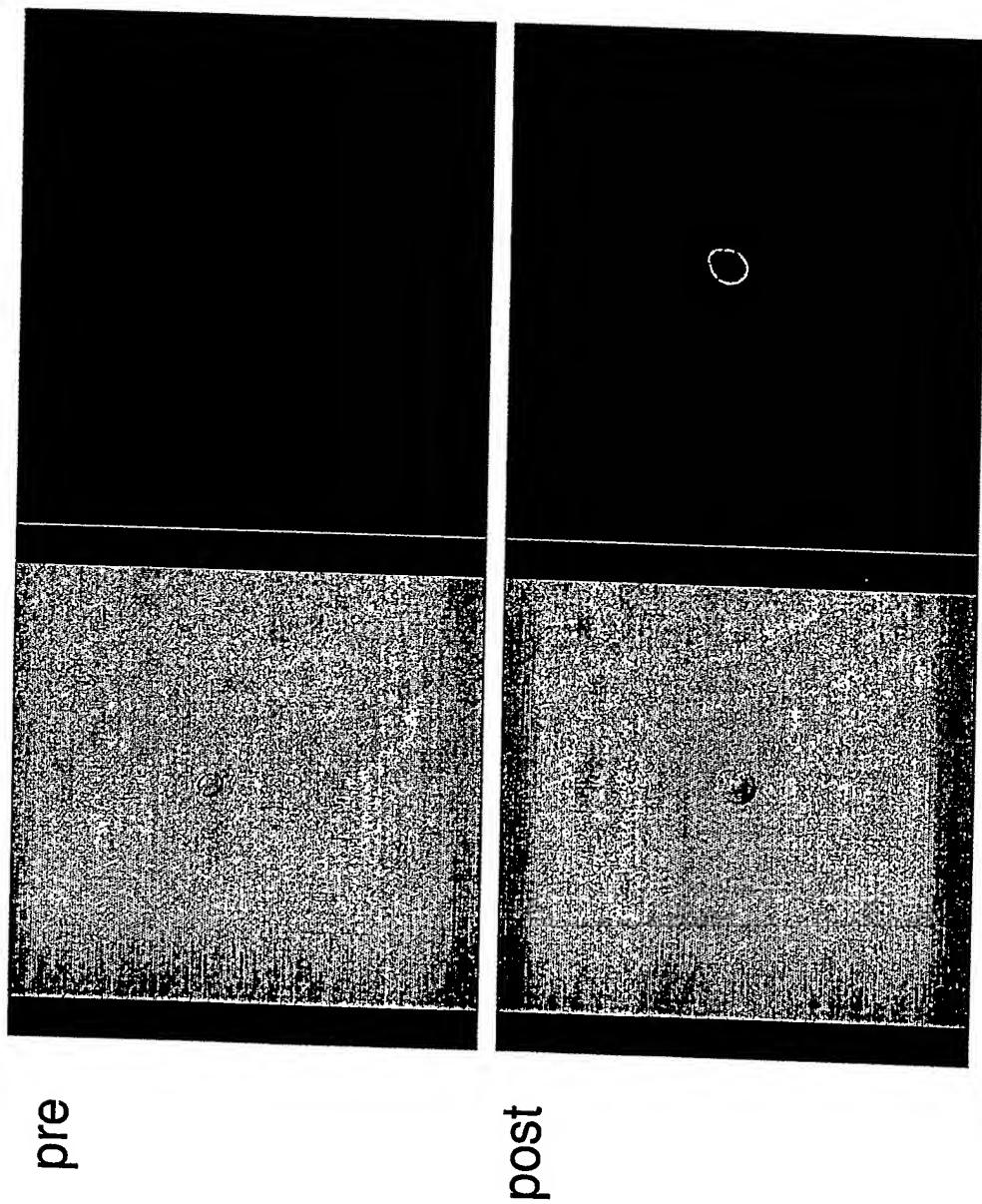


Fig.17 A B
 1 2 3 4 5 6

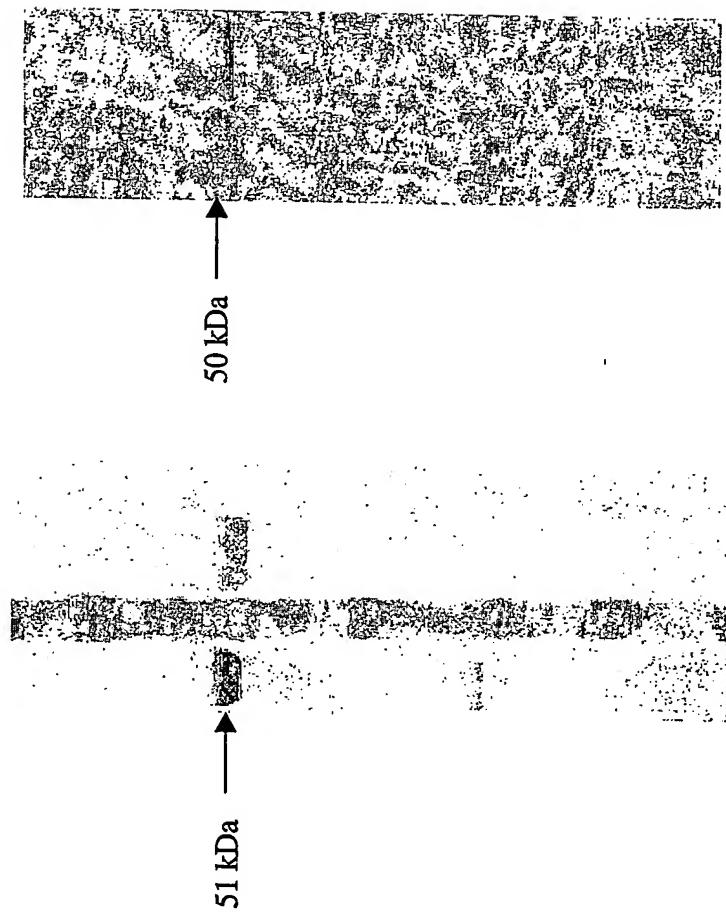


Figure 18**BLAST OF SEQ ID NO:36 AGAINST:**

Candida orf:

>orf19_7080 orf10262:179916-178795:e 1122 bp, 373 aa, contig 244073 bp
Length = 1122

Score = 335 bits (860), Expect = 1e-92
Identities = 185/368 (50%), Positives = 246/368 (66%), Gaps = 9/368 (2%)
Frame = +1

Query: 2 VTTYNILVLPGDGIGPEVMTEAVKVLKFEN----EHRKFNLRQELIGGCSIDAHGKSVT 57
V T I VLPGD +G E++ EA+KVLK E + +F+ + LI GG +IDA G +
Sbjct: 7 VKTKTITVLPGDHGVTIEVNEAIKVLKAIEAATPYQKIQFDFKHHLLIGGAAIDATGVPLP 186

Query: 58 EEVKKALESDAVLFAAVGGPKWDHIRRGLEDGPEGGLLQLRKAMDIYANLRPCSASSPSA 117
++ ++A SDAVL AVGGPKW G PE GLL++RK +++YAN+RPC+ +S S
Sbjct: 187 DDALESAKSSDAVLLGAVGGPKWG---TGTVRPEQGLLKIRKELNLYANIRPCNFASDSL 357

Query: 118 SIAKEFSPFRQEVEVIEGVDFVVVRENCGGAYFGKKIEEEDY----AMDEWGYSEREIQRI 172
E SP + EV++G + ++VRE GG YFG++ E+E+ A D Y+ E+ RI
Sbjct: 358 L---ELSPPLKAEVVKGTNLIIIVRELVGGIYFGERQEQQESEDKKTAWDTEKYTVDEVTRI 528

Query: 173 TRLSAEIALRHNPWPVISLDKANVLASSRLWRRVVEKTMTEYQPQVKLVHQLADSASLI 232
TR++A +AL+HNPP P+ SLDKANVLASSRLWR+ V+K ++ E+P + + HQL DSA++I
Sbjct: 529 TRMAAFMALQHNPLPIWSLDKANVLASSRLWRKTVDKVISEEFPALSVQHQLIDSAAMI 708

Query: 233 LATNPRALNGVILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYEPFH 292
L NP LNG+I+ N FGD+ISD+A I G+LG+LPSASL LP GLYEP H
Sbjct: 709 LIQNPTKLNGIIITSNMFQDIISDEASVIPGSLGLLPSASLASLPD--TNTAFGLYEPCH 882

Query: 293 GSAPTIAGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRT PDLGGKSG 352
GSAP + N NP+A IL A M R SLD EA+ +E+AV+ VLD+GIRT DL G S
Sbjct: 883 GSAPDLPA-NKVNPPIATILSAASMLRLSLDCVKEAEALEEAVKQVLDGIRTADLRGTSS 1059

Query: 353 TNEVGDAI 360
T EVGDAI
Sbjct: 1060TTEVGDAI 1083

Candida seq orf10262:179916-178795

1

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LGAVGGPKWGTGTVRPEQGLLKIRKELNLYANIRPCNFASDSLLELSPLKAEVVKGTNLIIIVRELVGGIYFGER
QEQQESEDKKTAWDTEKYTVDEVTRITRMAAFMALQHNPLPIWSLDKANVLASSRLWRKTVDKVISEEFPALS
VQHQLIDSAAMILIQNPTKLNGIIITSNMFQDIISDEASVIPGSLGLLPSASLASLPDTNTAFGLYEPCHGSAP
DLPANKVNPIATILSAASMLRLSLDCVKEAEALEEAVKQVLDGIRTADLRGTSS1060TTEVGDAI

Figure 19**BLAST OF SEQ ID NO:36 AGAINST:**

Elrond pep

A. nidulans

>AnrP4374925 LE3B ASPNG 3-isopropylmalate dehydrogenase B (Beta-IPM
dehyd
Length = 370

Score = 597 bits (1540), Expect = e-171

Identities = 295/364 (81%), Positives = 326/364 (89%), Gaps = 1/364 (0%)

Query: 4 TYNILVLPGDGIGPEVMTEAVKVLKFENEHRKFNLRQELIGGCSIDAHGKSVTEEVKKA 63
+YNILVLPGDGIGPEVM EA K+L +F +F + ELIGGCSID HGKSVT+ V A
Sbjct: 5 SYNILVLPGDGIGPEVMAEATKILSLFNTSTVRFRTQTELIGGCSIDTHGKSVTQAVLDA 64

Query: 64 ALESDAVLFAAVGGPKWDHIRRGLDGPEGGLLQLRKAMDIYANLRPCSASSPSASIAKEF 123
A+ SDAVLFAAVGGPKWDHIRRGLDGPEGGLLQ+RKAMDIYANLRPCS SPS IA++F
Sbjct: 65 AVSSDAVLFAAVGGPKWDHIRRGLDGPEGGLLQVRKAMDIYANLRPCSVDSPSREIARDF 124

Query: 124 SPFRQEVIEWGVDVVVRENCGGAYFGKKIEEEDYAMDEWGYSEREIQRITRLSAEIALRH 183
SPFRQ+VIEGVDFVVVRENCGGAYFGKK+EE+DYAMDEWGYS EIQRITRLSAE+ALRH
Sbjct: 125 SPFRQDVIEGVDFVVVRENCGGAYFGKKVEEDDYAMDEWGYSASEIQRITRLSAELALRH 184

Query: 184 NPPWPVISLDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLILATNPRALNGV 243
+PPWPVISLDKANVLASSRLWRRVVEKTM+ EYPQVKLVHQLADSASLI+ATNPRALNGV
Sbjct: 185 DPPWPVISLDKANVLASSRLWRRVVEKTMSEYPQVKLVHQLADSASLIMATNPRALNGV 244

Query: 244 ILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSE-TRKRTNGLYEPTHGSAPTIAGQN 302
ILADNTFGDM+SDQAGS+VGTLGVLPASLDGLP +++ +GLYEPTHGSAPTIAG+N
Sbjct: 245 ILADNTFGDMVSDQAGSLVGTGLGVLPASLDGLPKPGEQRKVHGLYEPTHGSAPTIAGKN 304

Query: 303 IANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSGTNEVGDAIVA 362
IANP AMILCVALMFRYS +ME EA++IE AV+ VLD GIRT DLGG +GT E GDA+VA
Sbjct: 305 IANPTAMILCVALMFRYSFNMEAEARQIEAAVRTVLDKGIRTSIDLGGSTGTREFGDAVVA 364

Query: 363 ALQG 366
AL+G
Sbjct: 365 ALKG 368

>AnrP4374925 niger seq

MSEKSYNILVLPGDGIGPEVMAEATKILSLFNTSTVRFRTQTELIGGCSIDTHGKSVTQA
VLDAAVSSDAVLFAAVGGPKWDHIRRGLDGPEGGLLQVRKAMDIYANLRPCSVDSPSREI
ARDFSPFRQDVIEGVDFVVVRENCGGAYFGKKVEEDDYAMDEWGYSASEIQRITRLSAEL
ALRHDPWPVISLDKANVLASSRLWRRVVEKTMSEYPQVKLVHQLADSASLIMATNPRALNGV
ILADNTFGDMVSDQAGSLVGTGLGVLPASLDGLPKPGEQRKVHGLYEPTHGSAPTIAGKN
AGKNIANPTAMILCVALMFRYSFNMEAEARQIEAAVRTVLDKGIRTSIDLGGSTGTREFGDAVVA
AVVAALKGEL

Figure 20**BLAST OF SEQ ID NO:36 AGAINST:**

BLASTP:temp_job2_pep_6_AnRP3711474
>AnRP3711474 hypothetical protein [Aspergillus oryzae]
 Length = 364

Score = 375 bits (963), Expect = e-104
 Identities = 195/367 (53%), Positives = 260/367 (70%), Gaps = 10/367 (2%)

Query: 2 VTTYNILVLPGDGIGPEVMTEAVKVLKVFE-NEHRKFNLRQELIGGCSIDAHGKSVTEEV 60
 +++YNI+V GD GPEV EA+KVL+ E N FNL+ L+GG SIDA G +T+E
 Sbjct: 1 MSSYNIVVFGGDHCGPEVTAEEAIKVLRAVEKNRDVTFNLQDHLLGGASIDATGSPLTDEA 60

Query: 61 KKAALESDAVLFAAVGGPKWDHIRGLDGPEGGLLQLRKAMDIYANLRPCSASSPSASIA 120
 AA +DAVL A+GGPKW G PE G+L+LRK M + NLRPC+ ++PS
 Sbjct: 61 LNAAKNADAVLLGAIGGPKWG---TGAVRPEQGILKLRKEMGTFGNLRPCNFAAPSLV-- 115

Query: 121 KEFSPFRQEVIEGVDFVVVRENCGGAYFGKKIEEED--YAMDEWGYSEREIQRITRLSAE 178
 E SP R +V GV+F ++RE GG YFG++ E++ YAMD YS EI+RI RL+A
 Sbjct: 116 -ESSPLRADVCRGVNFNIIRELTGGIYFGERKEDDGSGYAMDTEPYRSRAEIERIIRLAAH 174

Query: 179 IALRHNPWPVISLDKANVLASSRLWRRVVEKTMTTEYPQVKLVHQLADSASLILATNPR 238
 +AL+H+PP PV SLDKANVLA+SRLWR+VV + M E+PQ+K+ HQL DSA++I+ NPR
 Sbjct: 175 LALQHDPLPVWSLDKANVLATSRLWRKVVTTEVMAKEFPQLKIEHQLIDSAAMIMVKNPR 234

Query: 239 ALNGVILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYEPTHGSAPTI 298
 LNG+++ N FGD+ISD+A I G+LG+LPSASL G+P + + NG+YEP HGSAP I
 Sbjct: 235 QLNGIVVTSNLFGDIISDEASVIPGSLGLLPSASLSGIP-DGNSKVNGIYEPIHGSAPDI 293

Query: 299 AGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSGTNEVD 358
 AG+ I NPVA IL VA+M +YS + EA+ IE+AV V+++G+RT D+GGK+ T EVGD
 Sbjct: 294 AGKGIVNPVAAILSVAMMMQYSFGLFAEARAIEQAVSNVIESGVRTGDIGGKATTAEVGD 353

Query: 359 AIVAAALQ 365
 A+ A L+
 Sbjct: 354 AVAAELE 360

Oryzae seq >AnRP3711474
 MSSYNIVVFGGDHCGPEVTAEEAIKVLRAVEKNRDVTFNLQDHLLGGASIDATGSPLTDEA
 LNAAKNADAVLLGAIGGPKWGTGAVRPEQGILKLRKEMGTFGNLRPCNFAAPSLVESSPL
 RADVCRGVNFNIIRELTGGIYFGERKEDDGSGYAMDTEPYRSRAEIERIIRLAHLALQHD
 PPLPVWSLDKANVLATSRLWRKVVTTEVMAKEFPQLKIEHQLIDSAAMIMVKNPRQLNGIV
 VTSNLFGDIISDEASVIPGSLGLLPSASLSGIPDGNSKVNGIYEPIHGSAPDIAGKGIVN
 PVAAILSVAMMMQYSFGLFAEARAIEQAVSNVIESGVRTGDIGGKATTAEVGDAVAAELE
 KLLK

Figure 21**BLAST OF SEQ ID NO:36 AGAINST:**

BLASTP:temp_job2_pep_9_AnrP4379986
>AnrP4379986 conserved hypothetical protein [Aspergillus nidulans
 FGSC A4
 Length = 357

Score = 149 bits (376), Expect = 1e-36
 Identities = 113/369 (30%), Positives = 186/369 (49%), Gaps = 27/369 (7%)

Query: 1 MVTTYNILVLPGDGIGPEVMTEAVKVLKFENEHRKFNLRQELIGGCS--IDAHGKSVTE 58
 M TY I +P DGIGPEV+ V VLK ++ + F+L + S A GK ++
 Sbjct: 1 MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQSFSLDFTHLDWSSETFKATGKYIPD 60

Query: 59 EVKKAALESDAVLFAAVGGPKW-DHIRRGLDGPEGGLLQLRKAMDIYANLRPCSASSPSA 117
 + ++DA+LF AVG P DHI G L + + YAN+R P+
 Sbjct: 61 GGLEVKKNDAILFGAVGAPDVPDHISLW----GLRLAICQPFQQYANVR----PTR 109

Query: 118 SIAKEFSPFRQEVIEGVDFVVVRENCGGAYFGK-----KIEEEDYAMDEWGYSEREIQRI 172
 + SP R+ +D+V+VREN G Y G+ + + A + +S + ++RI
 Sbjct: 110 VLRGTQSPLRKCNTGDDWVIVRENSEGEYAGQGGRSHRGHPWEVATEVAIFSRQGVERI 169

Query: 173 TRLSAEIALRHNPWPVISLDKANVLASSRLWRRVVEKMTTEYPOVKLVHQLADSASLI 232
 R + E A + P + + K+N + + V + ++P+V + L D+ +
 Sbjct: 170 MRFAFETAAK-RPRKLLTVVTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTR 228

Query: 233 LATNPRALNGVILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYEPHT 292
 + P +L+ I+A N D++SD A ++ G++G+ P+++LD ++ ++EP H
 Sbjct: 229 MVLKPESLD-TIVASNLHADILSDLAAALAGSIGIAPTSNLD----PTRQNPMSFEPIH 282

Query: 293 GSAPTIAGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSG 352
 GSA I G+ IANPVA A M + L + A ++ + V+ V ++GI T DLGG +
 Sbjct: 283 GSAFDITGKGIANPVATFWTAAEMLEW-LGEKDAADKLMQCVESVCESGILTADLGGTAT 341

Query: 353 TNEVGDAIV 361
 T EV A+V
 Sbjct: 342 TKEVTSAVV 350

Nidulans seq >AnrP4379986
 MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQSFSLDFTHLDWSSETFKATGKYIPD
 GGLEVKKNDAILFGAVGAPDVPDHISLWGLRLAICQPFQQYANVRPTRVLRGTQSPLRK
 CNTGDDWVIVRENSEGEYAGQGGRSHRGHPWEVATEVAIFSRQGVERIMRFAFETAAKR
 PRKLLTVVTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTRMVLKPESLDTIV
 ASNLHADILSDLAAALAGSIGIAPTSNLDPTRQNPMSFEPIHGSAFDITGKGIANPVATF
 WTAEMLEWLGEKDAADKLMQCVESVCESGILTADLGGTATTKEVTSAVVEEINRLN

Figure 22**BLAST OF SEQ ID NO:36 AGAINST:**

>gnl|TIGR_222929|contig:1772:c_posadasii Coccidioides posadasii C735
 unfinished fragment of genome
 Length = 119053

Score = 286 bits (732), Expect(2) = e-128
 Identities = 146/233 (62%), Positives = 173/233 (74%), Gaps = 24/233 (10%)
 Frame = -3

Query: 160 AMDEWGYSTTEIQXXXXXXXXXXXXHDPPWPVISLDKANVLASSRLWRRVVENTISVEYP 219
 AMDEWGYST E+Q HDPPWPVIS+DKANVLASSRLWRRVVE T++ E+P
 Sbjct: 33806 AMDEWGYSTQEVRQRIARLAHVALRHDPPWPVISMDKANVLASSRLWRRVVEKTLTTEFP
 33627

Query: 220 QVKLVHQLADSASLIMATDPRVLNGVILADNTFGDMLSDQAGSLIGTLGVLPASLDGLP 279
 QVK HQLADSASLIMAT+PR LNGV+LADNTFGDMLSDQAGS++G+LGVLPSASL G+P
 Sbjct: 33626 QVKFSHQLADSASLIMATNPRSLNGVLLADNTFGDMLSDQAGSIVGSLGVLPASLSGIP
 33447

Query: 280 HPGKQE--KVRGLYEPTHGSAPT-----IAGKNIANPTAMILC 315
 +++ K LYEPTHGSAPT IAGKN+ANP AMILC
 Sbjct: 33446 GEKRKDGGKSYALYEPTHGSAPT*VNCDLWMINTARKANRLD*CRIAGKNVANPLAMILC
 33267

Query: 316 VSLMFYRFSNMEEARQIEDAVRAVLDRGLRTPDLGGNSSTQEFDAVVAALQ 368
 V++MFYRFSNME EA+ IE+AV A L+ G+RTPDLGG + T + G+A+VA ++
 Sbjct: 33266 VAMMFYRFSNMEPEAKAIENAVTATLEAGIRTPDLGGKAGTTDVGNAIVAHIK 33108

Query: 4 TRAYNILVLPGDGIGPEVMAEAIKVLRTFNSSSMQFHLQEELIGGISIDTHGHSVTQPXX 63
 ++ YNIL LPDGIGPE+MAEAIKVL+ F+S ++ F+L+ ELIGG SID HG +T
 Sbjct: 34383 SKTYNILTPGDGIGPEIMAEAIKVLQAFSSPNLFNLRNELIGGCSIDAHGTPITDAVK
 34204

Query: 64 XXXXXXXXXXXXXXXGGSKVDHIRRGLDGPEGGLLQVRKAMDIYANLRPCSVDVPSSREIAR 123
 GG K D RRGL+GPEGGLLQ+RK +D+Y N+RPCS DV ++R
 Sbjct: 34203 QAALESDAVLFASVGGPKWDSSRRGLEGPEGGLLQLRKVLDVYGNVRPCSTDV-CASVSR
 34027

Query: 124 DFSPFRQEVIEGVDFVVRENCGGAYFGKKVEEENY 159
 +FSP+R EV+EGVDFVV+RENCGGAYFGK VE+E+Y
 Sbjct: 34026 EFSPYRTEVVEGVDFVVLRENCGGAYFGKXVEDEDY 33919

Coccidioides 2

SKTYNILTPGDGIGPEIMAEAIKVLQAFSSPNLFNLRNELIGGCSIDAHGTPITDAVKQAALESDAVL
 FASVGGPKWDSSRRGLEGPEGGLLQLRKVLDVYGNVRPCSTDVCASVSREFSPYRTEVVEGVDFV
 VLRENCGGAYFGKXVEDEDYAMDEWGYSTQEVRQRIARLAHVALRHDPPWPVISMDKANVLASSR
 LWRRVVEKTLTTEFPQVKFSHQLADSASLIMATNPRSLNGVLLADNTFGDMLSDQAGSIVGSLVLP
 SASLSGIPGEKRKDGGKSYALYEPTHGSAPT*VNCDLWMINTARKANRLD*CRIAGKNVANPLAMILC
 VAMMFYRFSNMEPEAKAIENAVTATLEAGIRTPDLGGKAGTTDVGNAIVAHIK

Figure 23 SEQ ID NO:36 against: Cryptococcus >chr01b.b3501.031220.c11
 (289426 bp) Length = 289426

Score = 183 bits (465), Expect(3) = 3e-68 Frame = +3
 Identities = 113/258 (43%), Positives = 144/258 (55%), Gaps = 39/258 (15%)

Query: 148 FGKKIE--EEDYAMDEWGYSERETQRITRLSAEIALRHNPWPVVISLDKANVLASSRLWR 205
 FG++ E +E A D+ YS+ EI+RITR++A+IAL PP P+ S+DKANVLA+SRLWR
 Sbjct: 173334 FGERQETNDEGVAWDQCIYSKPEIERITRVAAQIALAAEPPPLPITSVDKANVLATSRLWR 173513

Query: 206 RVVEKTMTEYPQVKLVHQQLADSASLILATNPRALNGVILADNTFGDM----- 253
 + V + M EYPQ+KL HQL DSA++I+ NPR LNGV+L +N FGDM
 Sbjct: 173514 KTVSELMAKEYPQLKLEHQQLVDSAAMIMIANPRKLNGVLLTENMFGDM*VLSMVTKYRC* 173693

Query: 254 -----ISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYE-----PTHGS 294
 S A + L + P LP ++ HGS
 Sbjct: 173694 VCVVFLTKAPSSPAPLVSSLRLSPVPTLSSLPPWVMSRTSIFPFETYPN*PLCSIHGS 173873

Query: 295 APTIAGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAG-----IRTPDLG 348
 AP IAGQ IANP+ IL A+M RYSL EA IE+AVQ VLD+ RT DLG
 Sbjct: 173874 APDIAGQGIANPIGTTILSAAMMLRYSLGKGREAALIEQAVQKVLDSEAESGGFDYRTKDLG 174053

Query: 349 GKS GTNEVGDAIAVAAALQG 366
 G+ T EVGD +V L+G
 Sbjct: 174054 GQRSTKEVGDKVVEVLKG 174107

Query: 15 IGPEVMTTEAVKVLKFENEHR-KFNLRQELIGGCSIDAHGKSVTEEVKKALESDAVLFA 73
 IGPEV+ EAV+VL+ N K +L+ GG +ID HG + +E KA E+DAVL
 Sbjct: 172844 IGPEVVAEAVRVLETIVNHSDLKLDLKSYDFGGAAIDNHGVPLPDETLACKEADAVLMG 173023

Query: 74 A-----VGGPKWDHIRRLGLDPEGGLLQLRKAMDIYANLRPCSASSPS 116
 A VGGPKW G PE G+L+LRK + +YAN+RP A+ S
 Sbjct: 173024 ACDFLAIRIKS*TA*KGSVGGPKWGV---GPVRPEQGILKLRKELGLYANIRP--ANFAS 173188

Query: 117 ASIAKEFSPFROEVIEGVDFVVVRENCGG 145
 S+ K SP +++ G D +V+RE GG
 Sbjct: 173189 ESSLKRSPLKEDTARGTDIIVLRELIGG 173272

Query: 244 ILADNTFGDMISDQAGSIVGTLGVLPASLD-----GLPS---ETRKRTNGLYEPTH 292
 +L + +GD++SD + ++G LG+ PS ++ G PS K ++E H
 Sbjct: 238292 LLIPHRYGDLSDLASAGLIGGLTPSGNIGKVSLSHDYGSPSIELTGDK*DASIFEAVH 238471

Query: 293 GSAPTIAGQNIANPVAMILCVALMFR----- 318
 GSAP I G+ +ANP A++L +M R
 Sbjct: 238472 GSAPDIEGKGLANPTALLSSLLMMLR*VTQIPSIVPALYPSVPDHTHPLARNVADLFVH 238651

Query: 319 YSLDMETEAQRIEKA---VQG-----VLDAGIRTPDLGGKSGTNEVGD 358
 + + A +IEKA V G + + T DLGGK+GT E D
 Sbjct: 238652 RHMSLYELADKIEKAALSVSGTPWLHFTEMLIQVS*TIAEGKAITRDLGGKAGTKEYTD 238831

Query: 359 AIVAAAL 364
 AI++ L
 Sbjct: 238832 AILSKL 238849

Query: 95 LQLRKAMDIYANLRPCSASSPSASIAKEFSPFROEVIEGVDFVVVRENCGGAYFGKKIEE 154
 L LR+ ++AN+RPC SI +P+ + V+ V++REN G Y G IE
 Sbjct: 237609 LTLLRRTFSLFANVRPC-----VSIKGYKTPY-----DNVNTVLIRENTEGEYSG--IEH 237749

Query: 155 E 155
 E
 Sbjct: 237750 E 237752

Query: 5 YNILVLPGDGIGPEVMTEAVKVLK 28
 Y + ++PGDGIGPE+ ++ K
 Sbjct: 237256 YTVTLIPGDGIGPEIANSVKQIFK 237327

Query: 4 TYNILVLPGDGIG 16
 ++ I VLPGDGIG
 Sbjct: 172752 SFKITVLPGDGIG 172790

Figure 24
Clustalw of sequences of figure 18-22

```

! Sequence: BLASTP:temp_job2_pep_4_AnRP4374925 nidulans (see Figure 19)
! Sequence: BLASTP:temp_job2_pep_6_AnRP3711474 oryzae (see Figure 20)
! Sequence: BLASTP:temp_job2_pep_9_AnRP4379986 nidulans (see Figure 21)
! Sequence: USERPROTEIN:1_job6_1 candida (see Figure 18)
! Sequence: USERPROTEIN:2_job7_2 coccidioides (see Figure 22)

CLUSTAL W (1.82) multiple sequence alignment

temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

```

Figure 25 Continuation from Figure 24

```

temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2

```

:
 * : * . . . : * : : * : : * : : * : : * : : * : : * : :

GVLADNTFGDMMSDQAGSLVGTGLGVLPSSASLDGLP -- KPGEQRKVHGLY
 GIVVTSNLFGDILISDEAVLPGSLGLPSASLSGLP --- DGNNSKRVNGIY
 -TIVASNLLHDILSDEAVLPGSLGLPSASLSLP --- QNPSMF
 GIITSNMFGDILISDEAVLPGSLGLPSASLSLP --- DTN-TAFGLY
 GVLLADNTFGDMLSDQAGSLVGLPSASLSGLPGEKRDGKKSAYL
 : : . * . . * : * . : * : : * : : * : : * : : * : :

EPTHGSAPTIAGKNIANPTAMILCVAMFPRYSFMEAEARQIEAAVRTVL
 EPIHGSAPDIAGKGIVNPVAAILSVAMMYSFGLFAEARAEQAVSNVI
 EPIHGSAFDITGKGIANPVIATFWTAAMLEWLG-EKDAADKLMQCVESVC
 EPCHGSAPDLPan-KVNPIATILSAASMLRILSLDCVKEAEALLEAVQVL
 EPTHGSAPT ---
 ** * * * *

DKGIRTSIDLGGSTGTREFGDAVVAALKG
 ESGVRTGDIIGGKATTAEVGDAVAAELE-
 ESGILTADLGGTATTKEVTSAVV ---
 DSGIRTADLRGTSSTTEVDAI ---